

## SEQUENCE LISTING



<10> MOCKEL, BETTINA  
HERMANN, THOMAS  
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BINDER, MICHAEL  
PFEFFERLE, WALTER

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE SIGE GENE

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<141> 2001-08-24

<150> 60/295,009

<151> 2001-06-04

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<151> 2000-09-02

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<151> 2001-05-31

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gtcggtttca gtagtggact cgacataagt gcgaagatac tcgaaggcgt tactcacgcg 180

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ttcacaattg ccagaagatg cacaggatgt aatctagatt tccaagtgc agtggggcaa 300

a atg act tat atg aaa aag aag tcc cga gat gac gca ccc gtc gta atc 349

Met Thr Tyr Met Lys Lys Lys Ser Arg Asp Asp Ala Pro Val Val Ile

1

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10

15

gaa acc gtt caa gca gaa cat gct gaa gaa ctc acg ggc act gca gca 397

Glu Thr Val Gln Ala Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala

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Cm.t

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 Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala  
 35 40 45

gaa cat gca gat agc gtt tac cgc ctc gcg tac cgt ctt tcc ggc aac 493  
 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn  
 50 55 60

cag cac gat gct gaa gac ctg acc caa gaa aca ttc atg cgt gtc ttc 541  
 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe  
 65 70 75 80

cgc tcg ttg aag agc tac cag cca ggc acc ttt gag ggc tgg ctg cac 589  
 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His  
 85 90 95

cgc atc acc acc aac ttg ttc ctt gat atg gtt cgc cac cgc ggc aag 637  
 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys  
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atc cgc atg gag gcg ctg cct gaa gat tat gag cgc gtt ccg ggc aat 685  
 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn  
 115 120 125

gac atc acc cca gag cag gca tac acc gaa gct aac ctt gac cca gct 733  
 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala  
 130 135 140

ctg cag gca gcc ctc gat gag ttg agc cca gac ttc cgc gtg gca gtg 781  
 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val  
 145 150 155 160

atc ctc tgt gat gtt gtt ggt atg agc tat gac gaa atc gca gag acc 829  
 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr  
 165 170 175

ctc gga gtg aaa atg ggt acc gtg cgt tcc cgt att cac cgt gga cgc 877  
 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg  
 180 185 190

agc cag ctt cgt gca agt ttg gaa gct gca gca atg acc agc gag gaa 925  
 Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu  
 195 200 205

gtt tct ttg ttg gtt cca acc cac taaagttggt gtgttttctg acacgacaaa 979  
 Val Ser Leu Leu Val Pro Thr His  
 210 215

cgcaaatgtc gtgtcatttt tgcagctcag tgcattattt tgggggttcgt ggtgcggaca 1039

gggaacttat cacaggcgac atccgttttg agtagtaggt atcttgata agaagttacc 1099

cacatccttg aaagtcgaga cacaggaggt catcggaaga tatgttcaat tccgacacca 1159

ccgcgaatct ccaagctaaa agtcgagatc gtgcaggatc taaagcaaag cgcagcaggc 1219

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<213> Corynebacterium glutamicum

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Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala  
35 40 45

Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn  
50 55 60

Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe  
65 70 75 80

Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His  
85 90 95

Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys  
100 105 110

Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn  
115 120 125

Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala  
130 135 140

Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val  
145 150 155 160

Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr  
165 170 175

Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg  
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Val Ser Leu Leu Val Pro Thr His  
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<212> DNA

<213> Corynebacterium glutamicum

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Cm.T

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&lt;223&gt; upstream region

&lt;400&gt; 3

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gtacgcggct gggggaatag ccggcctcgc ggaagagtgc tttggcctgg cgctgatgct 360
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&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

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&lt;223&gt; downstream region

&lt;400&gt; 4

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&lt;211&gt; 2086

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Cm.t

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agatgtgaag tacctacacg cattaagtgc aaatgaattc acaattgccca gaagatgcac 720  
aggatgtaat ctagatttcc caagttcagt ggggcaaaa atg act tat atg aaa aag 776  
Met Thr Tyr Met Lys Lys  
1 5

aag tcc cga gat gac gca ccc gtc gta atc gaa acc gtt caa gca gaa 824  
Lys Ser Arg Asp Asp Ala Pro Val Val Ile Glu Thr Val Gln Ala Glu  
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cat gct gaa gaa ctc acg ggc act gca gca ttc gat gct gga cag gca 872  
His Ala Glu Leu Thr Gly Thr Ala Ala Phe Asp Ala Gly Gln Ala  
25 30 35

gac atg cca aca tgg ggc gag cta gtc gca gaa cat gca gat agc gtt 920  
Asp Met Pro Thr Trp Gly Glu Leu Val Ala Glu His Ala Asp Ser Val  
40 45 50

tac cgc ctc gcg tac cgt ctt tcc ggc aac cag cac gat gct gaa gac 968  
Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn Gln His Asp Ala Glu Asp  
55 60 65 70

ctg acc caa gaa aca ttc atg cgt gtc ttc cgc tcg ttg aag agc tac 1016  
Leu Thr Gln Glu Thr Phe Met Arg Val Phe Arg Ser Leu Lys Ser Tyr  
75 80 85

cag cca ggc acc ttt gag ggc tgg ctg cac cgc atc acc acc aac ttg 1064  
Gln Pro Gly Thr Phe Glu Gly Trp Leu His Arg Ile Thr Thr Asn Leu  
90 95 100

ttc ctt gat atg gtt cgc cac cgc ggc aag atc cgc atg gag gcg ctg 1112  
Phe Leu Asp Met Val Arg His Arg Gly Lys Ile Arg Met Glu Ala Leu  
105 110 115

cct gaa gat tat gag cgc gtt ccg ggc aat gac atc acc cca gag cag 1160  
Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn Asp Ile Thr Pro Glu Gln  
120 125 130

gca tac acc gaa gct aac ctt gac cca gct ctg cag gca gcc ctc gat 1208  
Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala Leu Gln Ala Ala Leu Asp  
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Glu Leu Ser Pro Asp Phe Arg Val Ala Val Ile Leu Cys Asp Val Val  
155 160 165

ggt atg agc tat gac gaa atc gca gag acc ctc gga gtg aaa atg ggt 1304  
Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr Leu Gly Val Lys Met Gly  
170 175 180

acc gtg cgt tcc cgt att cac cgt gga cgc agc cag ctt cgt gca agt 1352  
Thr Val Arg Ser Arg Ile His Arg Gly Arg Ser Gln Leu Arg Ala Ser  
185 190 195

Al  
Cmit

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 200 205 210

acc cac taaagttggt gtgttttctg acacgacaaa cgcaaattgtc gtgtcatttt 1456  
 Thr His  
 215

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 35 40 45  
 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn  
 50 55 60  
 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe  
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 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His  
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 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys  
 100 105 110

AI  
 Cmt

Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn  
 115 120 125

Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala  
 130 135 140

Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val  
 145 150 155 160

Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr  
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Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg  
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Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu  
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AI  
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